SUPPLEMENTAL MATERIAL

Oresic et al., http://www.jem.org/cgi/content/full/jem.20081800/DC1

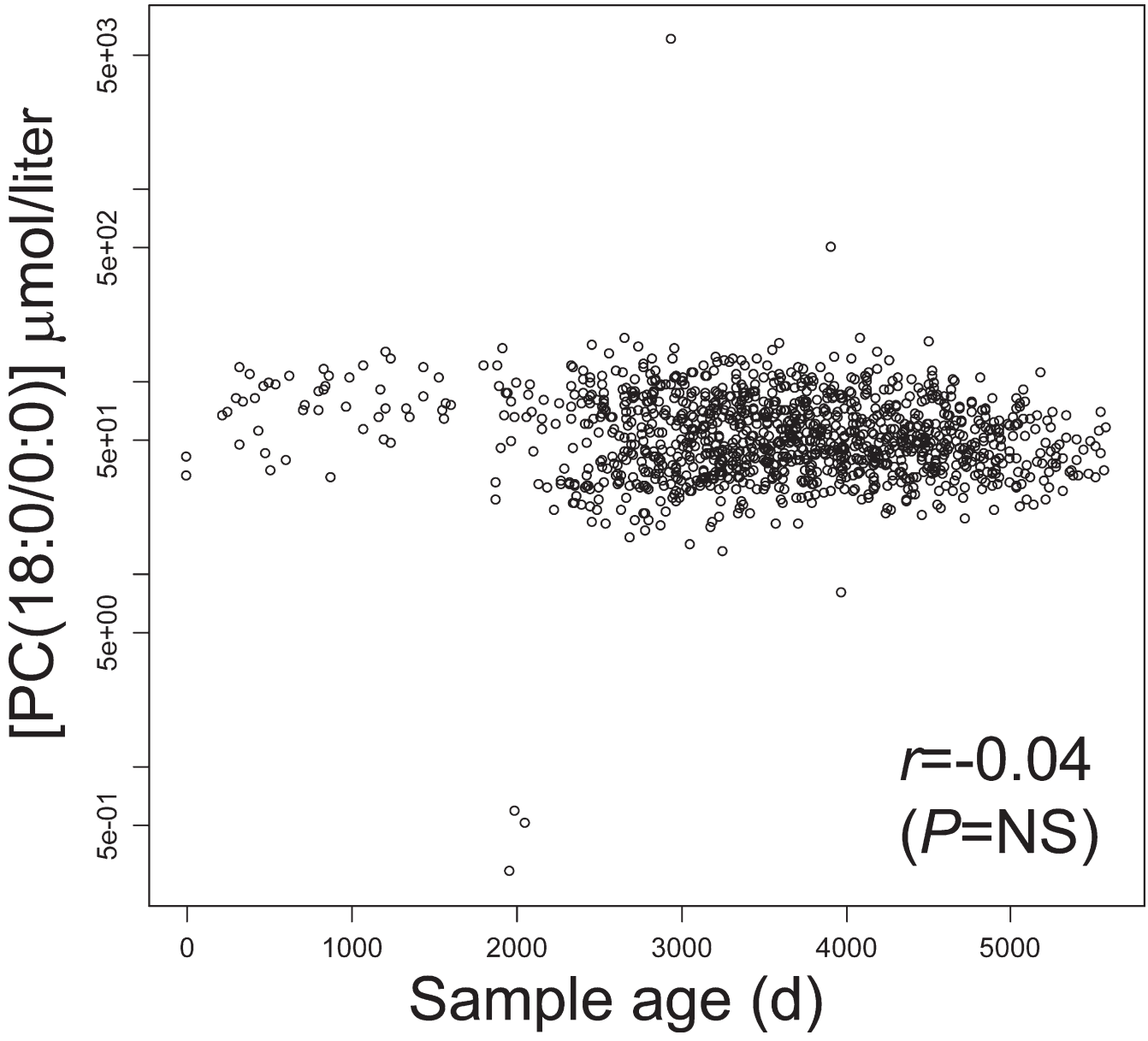

Figure S1. Levels of the lysoPC PC(18:0/0:0) as a function of sample age (storage time) across all 1,196 samples from the prospective series from DIPP and STRIP studies, analyzed by the UPLC/MS-based lipidomics platform. With the oldest samples analyzed by the lipidomics platform being >12 yr of age, the integrity of the samples and potential effect of lipid oxidation was clearly of potential concern, despite sample storage at −70°C and well controlled sample preparation protocols. As potential excessive sample age-related lipid oxidation caused by improper storage would lead to higher levels of lysophospholipids, we examined the levels of the most abundant lysoPC, PC(18:0/0:0), as dependent on sample age across all 1,196 samples analyzed. We found no significant trend in lysoPC levels with age, as calculated by Pearson correlation, thus confirming that our findings are not confounded by sample age (storage time).

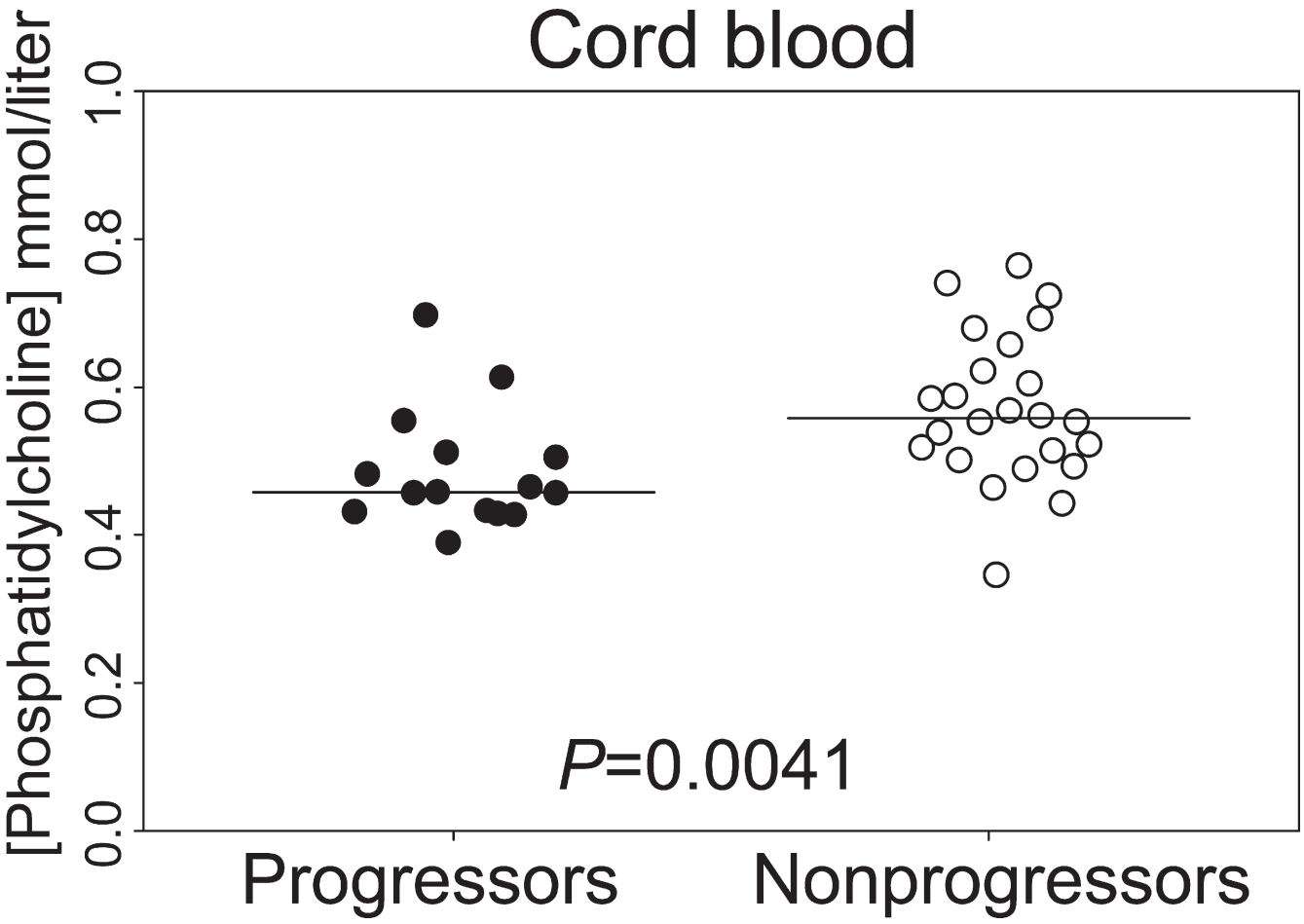

Figure S2. Total PC levels in cord blood from progressors and nonprogressors shown separately for each subject. The median lines are marked. Total PC level is calculated as the sum of concentrations across all 62 detected PC species in cord blood.

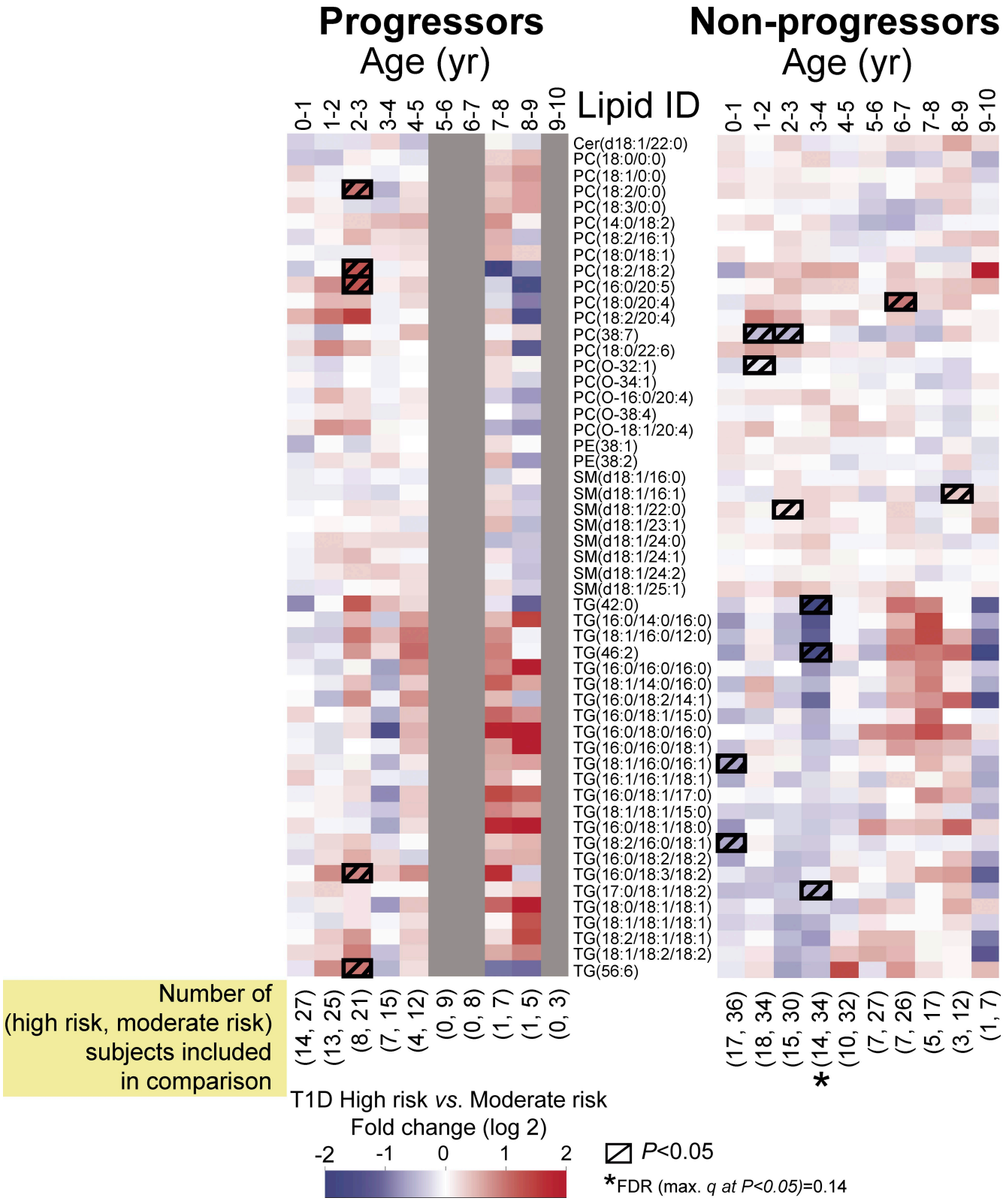

Figure S3. Comparison of serum lipidomes between children with the high-risk HLA genotype and those with moderate-risk HLA genotypes as defined in Table I. The comparisons are shown separately for progressors and nonprogressors. The age groups are divided into groups covering 1-yr cohorts. Only one sample per subject, closest to the mean age within the time window, is used in each comparison. Except for the age cohort of 3–4 yr in nonprogressors, none of the false discovery rates were <0.25. Gray columns indicate the age cohorts where no high-risk subjects were included.

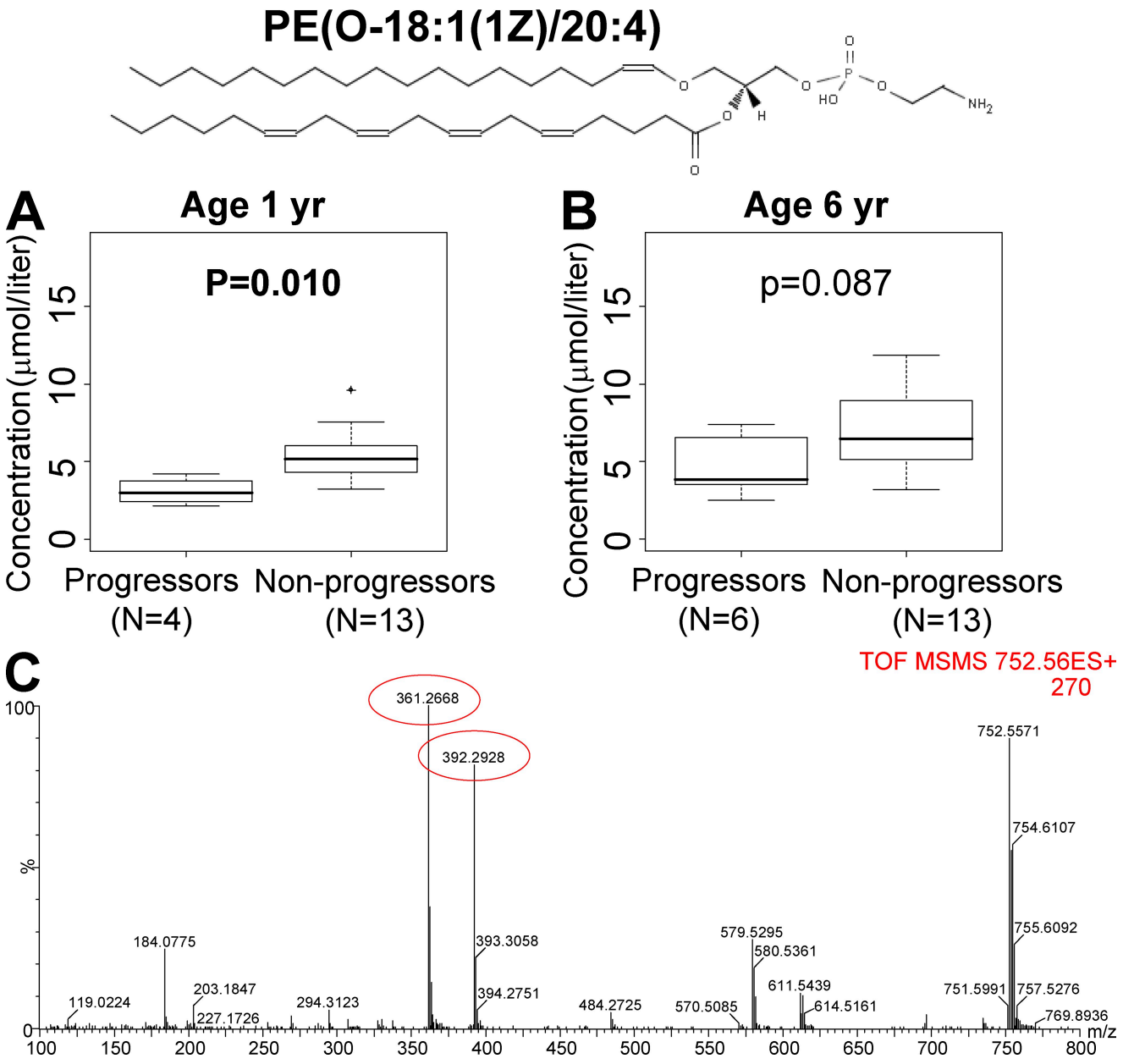

Figure S4. Early age differences between progressors and nonprogressors for the ethanolamine plasmalogen PE(O-18:1(1Z)/20:4), which was detected in one out of four analytical runs (batch 1) and, thus, was not included in the analyses shown in the paper. (A and B) The plasmalogen levels are shown for children with ages between 315 and 405 d (A) and with ages between 1,980 and 2,340 d (B). The box itself contains the middle 50% of the data. The top edge (hinge) of the box indicates the 75th percentile of the data set, and the bottom hinge indicates the 25th percentile. The line in the box indicates the median value of the data. The ends of the vertical lines or "whiskers" indicate the minimum and maximum data values, unless outliers are present in which case the whiskers extend to a maximum of 1.5× the interquartile range. The points outside the ends of the whiskers are outliers or suspected outliers. (C) ESI^+ MS/MS spectrum of PE(O-18:1(1Z)/20:4) identified based on characteristic fragments as previously described (Zemski Berry, K.A., and R.C. Murphy. 2004. *J. Am. Soc. Mass Spectrom.* 15:1499–1508).

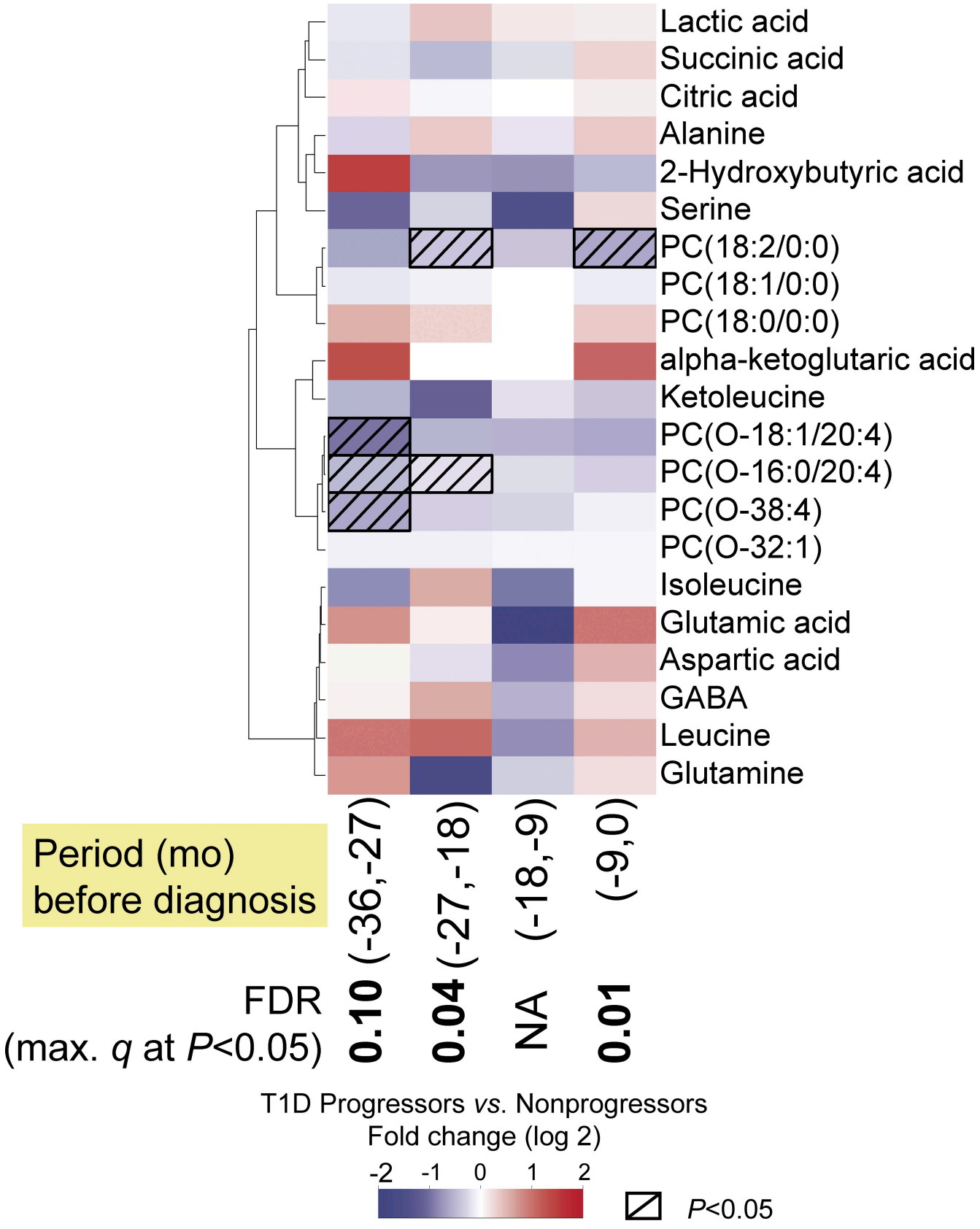

Figure S5. Differences in selected metabolite concentrations between the progressors to type 1 diabetes and nonprogressors within the four 9-mo intervals before disease diagnosis in the progressors.

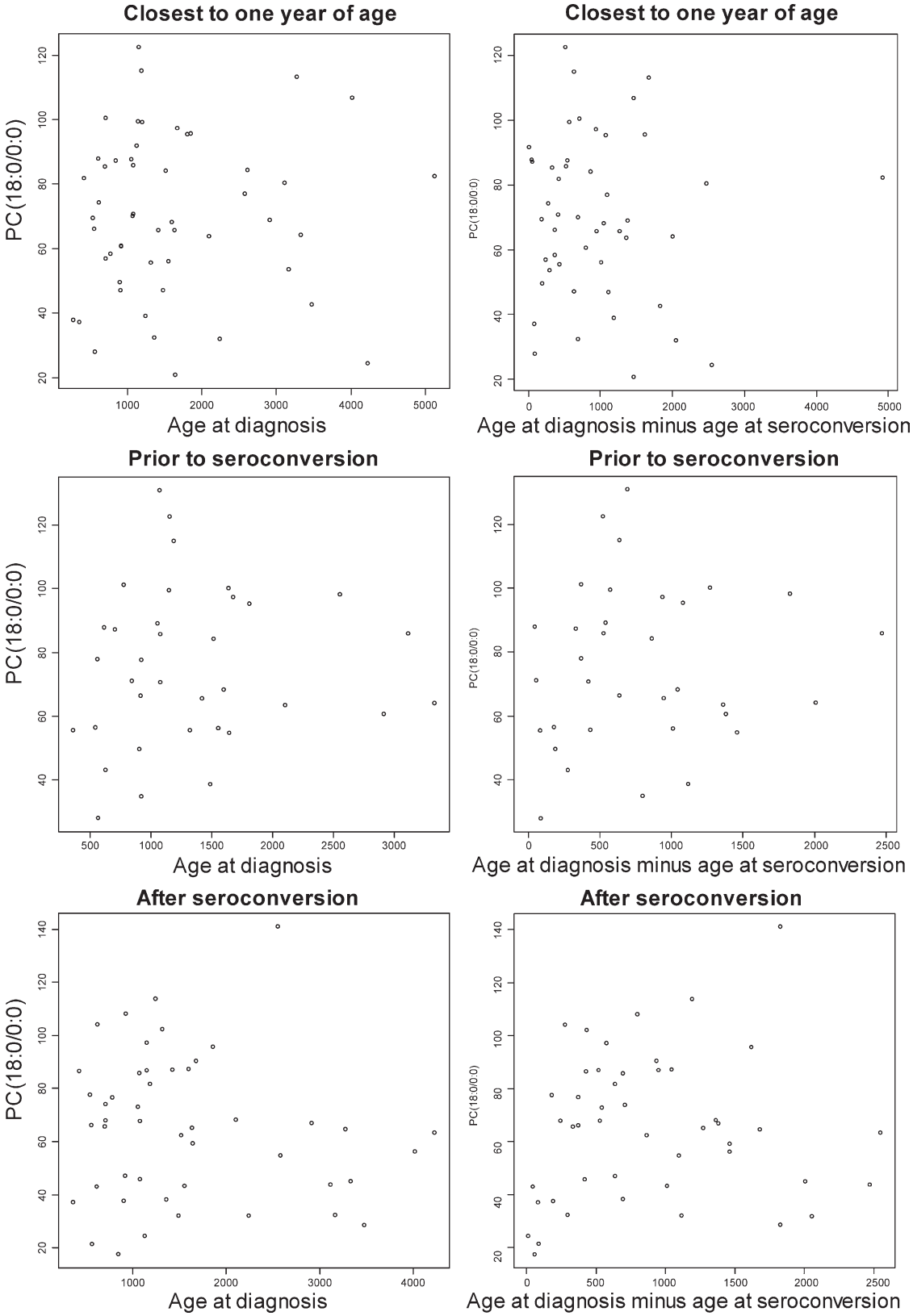

Figure S6. Associations of the lysoPC PC(18:0/0:0) concentrations with the rates of progression to overt type 1 diabetes. None of the associations were significant ($P < 0.05$) using the Spearman rank correlation.

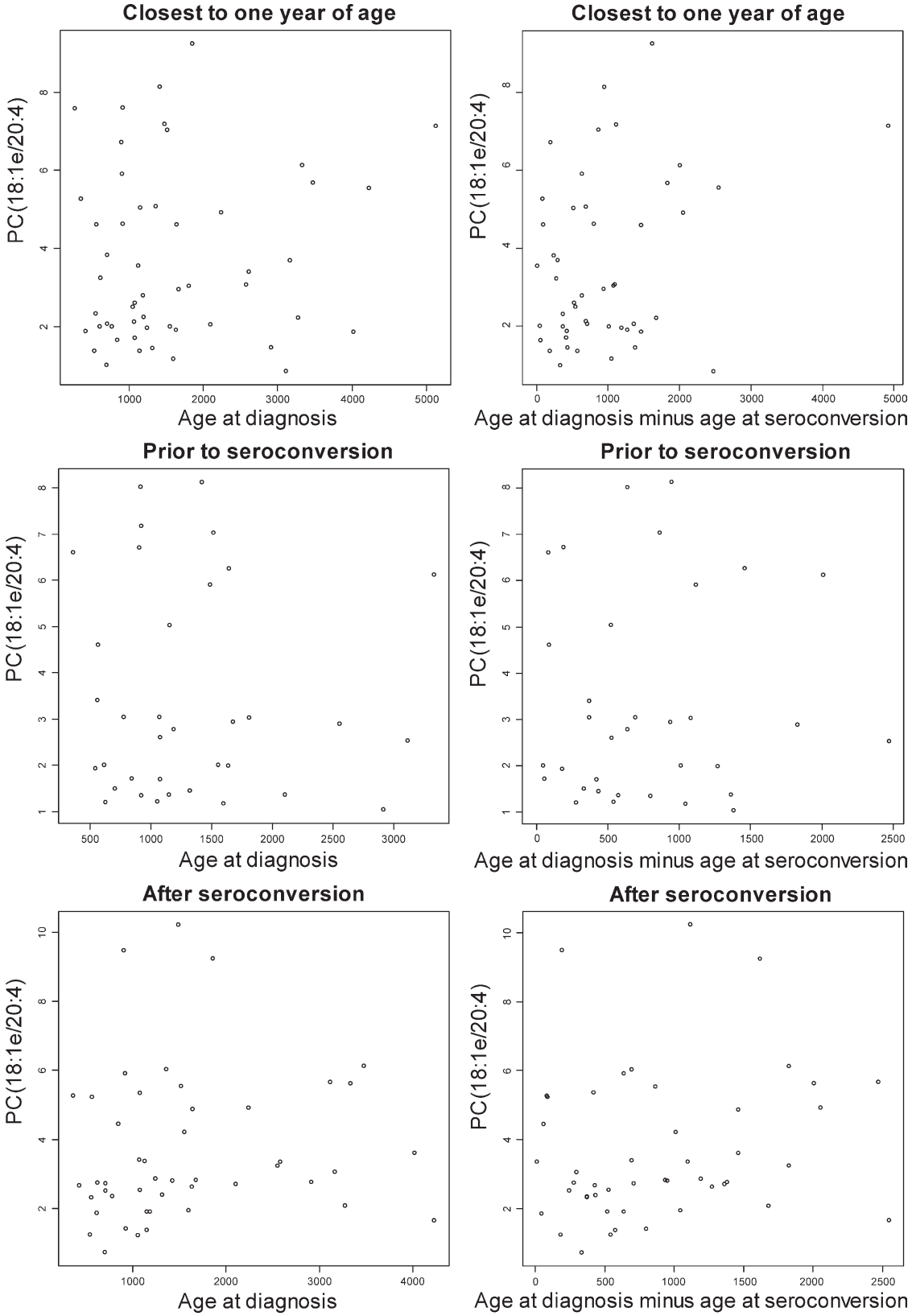

Figure S7. Associations of the ether PC PC(O-18:1/20:4) concentrations with the rates of progression to overt type 1 diabetes. None of the associations were significant ($P < 0.05$) using the Spearman rank correlation.

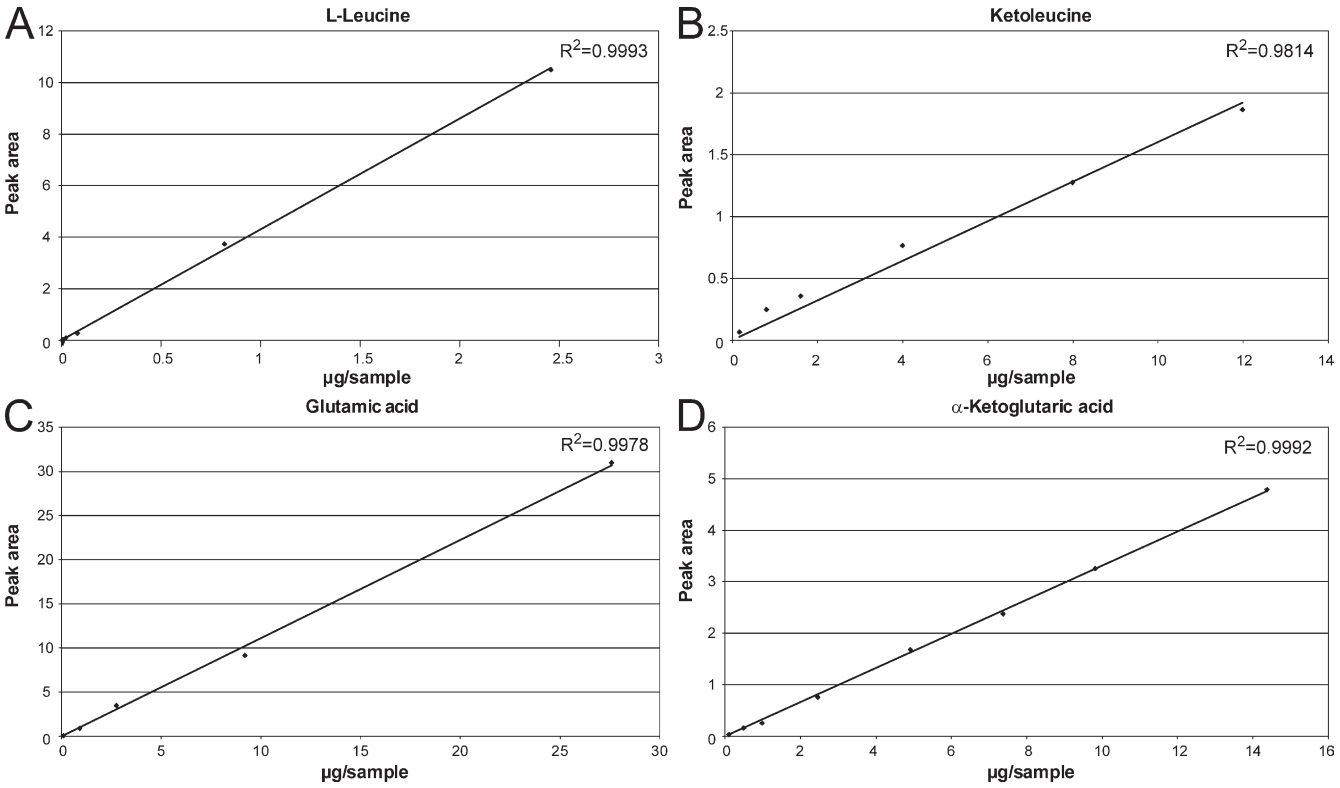

Figure S8. Response curves obtained with the GCxGC–TOF/MS platform and measured from nonextracted water solutions of pure compounds. (A) Leucine. (B) Ketoleucine. (C) Glutamic acid. (D) α-ketoglutarate

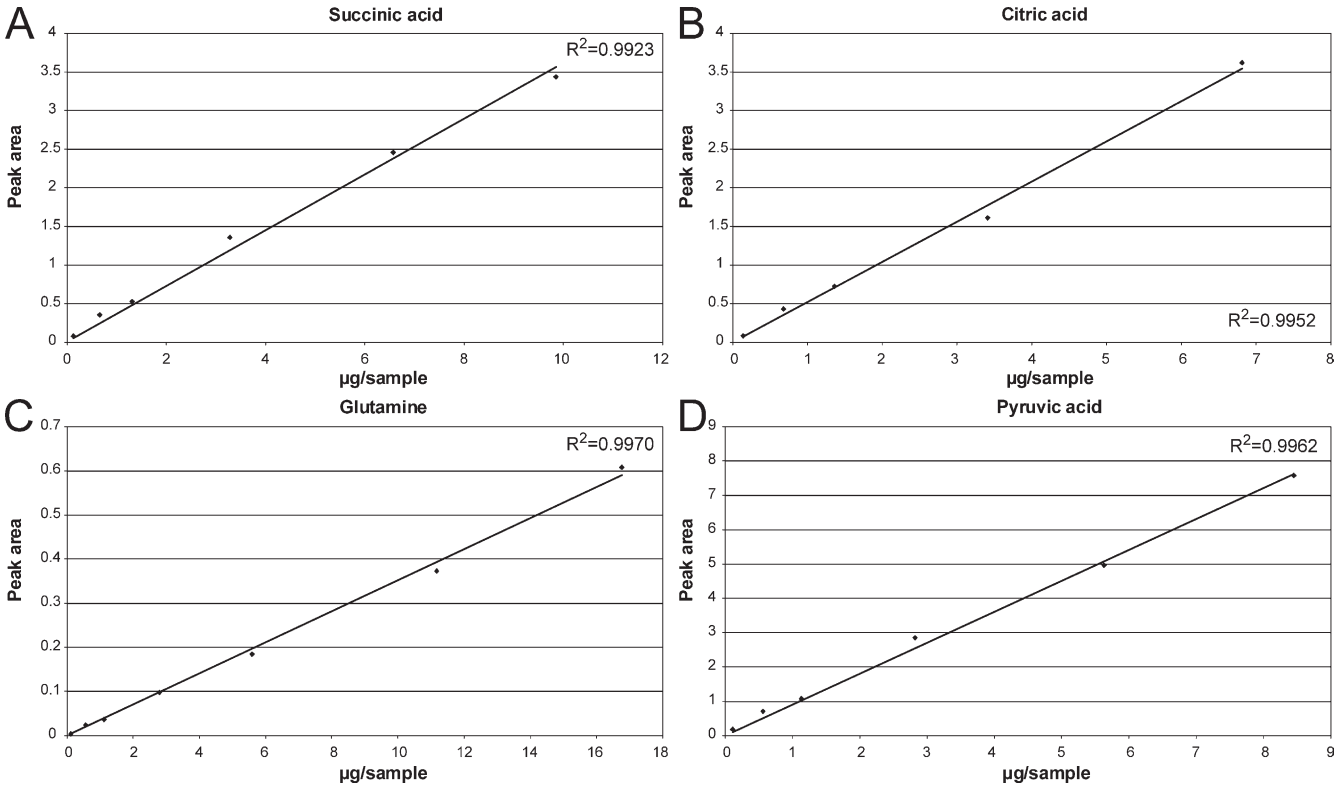

Figure S9. Response curves obtained with the GCxGC-TOF/MS platform and measured from nonextracted water solutions of pure compounds. (A) Succinic acid. (B) Citric acid. (C) Glutamine. (D) Pyruvate.

Table S1. Overview of the four analytical batches and included subjects

Analytical batch	City of birth	Study	Year of birth	Age at diagnosis	Number of progressors[a]	Number of nonprogressors[b]	Number of samples[c]
1	Turku	DIPP	1994-2001	1–11 yr	13	26	441
2	Turku	DIPP	1996-1999	1–6 yr	10	13	185
3	Oulu	DIPP	1996-2001	1–8 yr	27	28	483
4	Turku	STRIP	1990	3–13 yr	6	6	87

Lipidomic analysis was performed on all batches, whereas the GCxGC-TOF/MS analysis was performed on analytical batch 1.
[a]Total number of progressors: 56.
[b]Total number of nonprogressors: 73.
[c]Total number of samples: 1,196.